

Attorney Docket No: SEL-00104.P.1-US

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Yu

Examiner: To be determined

Group Art Unit: To be determined

Application Number: To be determined

Filed: Herewith

For: COMPOSITIONS AND
METHODS FOR IDENTIFYING
POLYPEPTIDES AND NUCLEIC
ACID MOLECULES

Assistant Commissioner for Patents
Washington D.C., 20231

Sir,

PRELIMINARY AMENDMENT NO. 1

Prior to examination, please amend the application as provided below. This amendment is made to economize on USPTO fees. Support for this amendment is provided throughout the specification and claims as originally filed.

IN THE CLAIMS

Please cancel all of the claims, claims 1 through 110.

Please add the following claims, claims 111 through 169.

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111. A nucleic acid molecule, comprising a nucleotide sequence that:
 - a) comprises a moiety binding region; and
 - b) encodes an interacting domain,wherein said interacting domain directly or indirectly binds with said moiety binding region.
112. The nucleic acid molecule of claim 111, wherein said nucleic acid molecule comprises ssRNA or dsRNA.
113. The nucleic acid molecule of claim 111, further comprising or encoding at least one random sequence or at least one sequence of interest.
114. The nucleic acid molecule of claim 111, wherein said nucleic acid molecule comprises ssDNA.
115. The nucleic acid molecule of claim 114, further comprising or encoding at least one random sequence or at least one sequence of interest.
116. The nucleic acid molecule of claim 111, wherein said nucleic acid molecule comprises dsDNA.
117. The nucleic acid molecule of claim 116, further comprising or encoding at least one random sequence or at least one sequence of interest.
118. The nucleic acid molecule of claim 111, further comprising or encoding a spacer region.

119. The nucleic acid molecule of claim 111, further comprising or encoding at least one expression control sequence.
120. The nucleic acid molecule of claim 111, further comprising or encoding at least one start codon.
121. The nucleic acid molecule of claim 111, wherein said nucleic acid molecule is operably linked to said interacting domain.
122. The nucleic acid molecule of claim 121, wherein said interacting domain binds directly or indirectly with said moiety binding region.
123. The nucleic acid molecule of claim 111, wherein said nucleic acid molecule is operably linked to a polypeptide encoded by said random sequence or said sequence of interest.
124. The nucleic acid molecule of claim 121, wherein said moiety binding region binds with said interacting domain to form a moiety binding region/interacting domain complex.
125. The nucleic acid molecule of claim 123, wherein said moiety binding region is operably linked to said interacting domain to form a moiety binding region/interacting domain complex.
126. The nucleic acid molecule of claim 124, wherein said moiety binding region/interacting domain complex reduces the efficiency of translation of said nucleic acid molecule.
127. The nucleic acid molecule of claim 124, wherein said interacting domain comprises a polypeptide.

128. The nucleic acid molecule of claim 124, wherein said polypeptide encoded by said random sequence is bound with a substance of interest.
129. The nucleic acid molecule of claim 128, wherein said substance of interest is on a solid support or in solution.
130. The nucleic acid molecule of claim 128, wherein said substance of interest comprises at least one organic molecule, an inorganic molecule, a polymer, a polypeptide, a nucleic acid molecule, a ribozyme, a lipid, a carbohydrate, a small molecule, a biomacromolecule or a drug.
131. A library of nucleic acid molecules of claim 111.
132. The library of nucleic acid molecules of claim 131, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.
133. A library of nucleic acid molecules of claim 121.
134. The library of nucleic acid molecules of claim 133, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.
135. A library of nucleic acid molecules of claim 133.
136. The library of nucleic acid molecules of claim 135, wherein said library comprises at least two different random sequences, at least two different sequences of interest or a combination of at least one random sequence and at least one sequence of interest.

137. The library of nucleic acid molecules of claim 130, wherein said library is contacted with at least one substance of interest.
138. The library of nucleic acid molecules of claim 137, wherein said at least one substance of interest is directly or indirectly bound on a solid support or in solution.
139. A method for identifying a nucleic acid molecule or sequence, comprising:
1. providing at least one nucleic acid molecule of claim 111;
 2. translating said nucleic acid molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence or a nucleic acid molecule of interest;
 3. contacting said at least one complex with at least one substance of interest;
 4. selecting at least one complex that binds with said at least one substance of interest; and
 5. identifying said random sequence or said nucleic acid sequence of interest or nucleic acid molecule of interest.
140. The method of claim 139, wherein said identifying comprising amplifying said random sequence or said nucleic acid sequence of interest or said nucleic acid molecule of interest.
141. The method of claim 139, wherein said substance of interest is on a solid support or in solution.
142. The method of claim 139, wherein said substance of interest is on or within a cell.

143. A nucleic acid molecule comprising a random sequence or nucleic acid sequence or nucleic acid molecule identified by the method of claim 139.
144. The method of claim 139, further comprising performing steps 1, 2, 3 and 4 reiteratively.
145. A method for identifying a nucleic acid molecule or sequence, comprising:
1. providing at least one nucleic acid molecule of claim 111;
 2. transcribing said nucleic acid molecule to a corresponding RNA molecule;
 3. translating said RNA molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence of interest or a nucleic acid molecule of interest;
 4. contacting said at least one complex with at least one substance of interest;
 5. selecting at least one complex that binds with said at least one substance of interest; and
 6. identifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest.
146. The method of claim 145, wherein said identifying comprising amplifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest.
147. The method of claim 145, wherein said substance of interest is on a solid support or in solution.
148. A nucleic acid molecule comprising a random sequence or nucleic acid sequence or nucleic acid molecule identified by the method of claim 145.

149. The method of claim 145, further comprising the step of sequencing the identified random sequence or nucleic acid sequence of interest or said nucleic acid molecule of interest.
150. The method of claim 145, further comprising performing steps 1, 2, 3, 4 and 5 reiteratively.
151. A method for identifying a polypeptide encoded by a random nucleic acid sequence or nucleic acid sequence of interest or nucleic acid molecule of interest, comprising:
1. providing at least one nucleic acid molecule of claim 111;
 2. translating said nucleic acid molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence of interest or a nucleic acid molecule of interest;
 3. contacting said at least one complex with at least one substance of interest;
 4. selecting at least one complex that binds with said at least one substance of interest; and
 5. identifying said polypeptide in said complex.
152. The method of claim 151, wherein said identifying comprises amplifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest or nucleic acid molecule of interest.
153. The method of claim 151, wherein said substance of interest is on a solid support or in solution.
154. The method of claim 151, wherein said substance of interest is on or within a cell.

155. The method of claim 151, wherein the nucleic acid sequence corresponding to the identified polypeptide is determined.
156. A polypeptide identified by the method of claim 155.
157. The method of claim 151, further comprising performing steps 1, 2, 3 and 4 reiteratively.
158. A method for identifying a polypeptide encoded by a random nucleic acid sequence or nucleic acid sequence of interest or nucleic acid molecule of interest in the nucleic acid, comprising:
1. providing at least one nucleic acid molecule of claim 111;
 2. transcribing said nucleic acid molecule to a corresponding RNA molecule;
 3. translating said RNA molecule to provide at least one complex, wherein said complex comprises a polypeptide operably linked to a random sequence or a nucleic acid sequence of interest or a nucleic acid molecule of interest;
 4. contacting said at least one complex with at least one substance of interest;
 5. selecting at least one complex that binds with said at least one substance of interest; and
 6. identifying said polypeptide in said complex.
159. The method of claim 158, wherein said identifying comprising amplifying said random sequence or nucleic acid sequence of interest or nucleic acid molecule of interest or nucleic acid molecule of interest.
160. The method of claim 158, wherein said substance of interest is on a solid support or in solution.

161. The method of claim 158, wherein the nucleic acid sequence corresponding to said identified polypeptide is determined.
162. A polypeptide identified by the method of claim 158.
163. The method of claim 158, further comprising performing steps 1, 2, 3, 4 and 5 reiteratively.
164. A method for identifying a test compound, comprising:
- a) contacting a target with a complex that:
 - 1) comprises a moiety binding region;
 - 2) encodes an interacting domain; and
 - 3) comprises a random sequence or a sequence of interest that encodes a polypeptide;wherein said interacting domain directly or indirectly binds with said moiety binding region;
 - b) identifying polypeptides bound with said target;
 - c) determining the structure of said polypeptide; and
 - d) identifying moieties that have structures that have space filling shapes that are similar to at least a portion of said polypeptide.
165. A test compound identified by method of claim 164.
166. A pharmaceutical composition identified by a method of claim 164.

167. A method for identifying a target, comprising:

- a) contacting a substance of interest with a complex that:
 - 1) comprises a moiety binding region;
 - 2) encodes an interacting domain; and
 - 3) comprises a random sequence or a sequence of interest that encodes a polypeptide;wherein said interacting domain directly or indirectly binds with said moiety binding region;
- b) identifying targets that bind with said complex.

168. A target identified by the method of claim 167.

169. A pharmaceutical target identified by the method of claim 167. - -

Accordingly, claims 111 through 169 are pending upon entry of this Preliminary Amendment.

Applicants respectfully submit that the claims are ready for examination and in condition for allowance.

Respectfully submitted,

Date: March 28, 2001



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Date of Deposit: March 29, 2001

Assistant Commissioner for Patents
Washington DC 20231

Re: U.S. Utility Patent Application
Appl. No.: To be determined
Filed: Herewith
Entitled: Compositions and Methods for Identifying Polypeptides and
Nucleic Acid Molecules
Inventor: Yu
Our Ref.: SEL-00104.P.1-US

Sir:

The following documents are forwarded herewith for appropriate action by the United States Patent and Trademark Office:

1. One application, with a total of [128] pages, with [1] title page, [99] pages of disclosure, [4] pages of Sequence Listing, [16] pages of claims, with [110] claims, [1] page abstract, [7] sheets of figures, with [7] figures;

Entitled: **Compositions and Methods for Identifying Polypeptides and Nucleic Acid Molecules**

Named Inventor: **Zhongping Yu**

2. One Statement Claiming Small Entity Status – Small Business;
3. Utility Patent Application Transmittal (in duplicate);
4. Fee Transmittal (in duplicate);
5. One Declaration;

6. One Assignment Cover Sheet;
7. One Assignment;
8. Statement Under 37 C.F.R. 1.821(f) for Sequence Listing;
9. One Computer Readable Form of Sequence Listing;
10. One Preliminary Amendment;
11. One Return Post Card; and
12. Our Check Number 698 for \$746.00.

It is respectfully requested that the attached postcard be stamped with the filing date and unofficial application number and returned as soon as possible.

The following attorney is the attorney of record for prosecuting this application and transacting all business in the USPTO connected therewith:

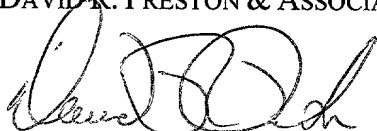
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Please charge any necessary additional fees or apply any credits to **Deposit Account number 501321** in the name of David R. Preston & Associates having **Customer Number 24232**.

Respectfully Submitted,
DAVID R. PRESTON & ASSOCIATES

A handwritten signature in black ink, appearing to read 'David R. Preston', written over the printed name.

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